

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
- (ii) TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
- (iii) NUMBER OF SEQUENCES: 59
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
(B) STREET: 699 Prince Street
(C) CITY: Alexandria
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22314-3187
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/523,894
(B) FILING DATE: 06-SEP-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 012712-165
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-836-6620
(B) TELEFAX: 703-836-2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: light variable domain of CE9.1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..420

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAC	ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCC	CCC	AGA	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Val	Ala	Ala	Pro	Arg			
-19				-15					-10						-5	
TGG	GTC	TTG	TCC	CAG	GTG	CAG	CTG	CAG	GAG	GCG	GGC	CCA	GGA	CTG	GTG	96
Trp	Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ala	Gly	Pro	Gly	Leu	Val	
			1				5						10			
AAG	CCT	TCG	GAG	ACC	CTG	TCC	CTC	ACC	TGC	AGT	GTC	TCT	GGT	GGC	TCC	144
Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	
	15						20					25				
ATC	AGC	GGT	GAC	TAT	TAT	TGG	TTC	TGG	ATC	CGC	CAG	TCC	CCA	GGG	AAG	192
Ile	Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	
30						35					40					
GGA	CTG	GAG	TGG	ATC	GGC	TAC	ATC	TAT	GGC	AGT	GGT	GGG	GGC	ACC	AAT	240
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	
45					50				55						60	
TAC	AAT	CCC	TCC	CTC	AAC	AAT	CGA	GTC	TCC	ATT	TCA	ATA	GAC	ACG	TCC	288
Tyr	Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	
			65					70					75			
AAG	AAC	CTC	TTC	TCC	CTG	AAA	CTG	AGG	TCT	GTG	ACC	GCC	GCG	GAC	ACG	336
Lys	Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	
			80					85					90			
GCC	GTC	TAT	TAC	TGT	GCG	AGT	AAT	ATA	TTG	AAA	TAT	CTT	CAC	TGG	TTA	384
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	
		95					100					105				
TTA	TAC	TGG	GGC	CAG	GGA	GTC	CTG	GTC	ACC	GTC	TCC					420
Leu	Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser					
110					115						120					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -19 -15 -10 -5
 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys
 1 5 10
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
 15 20 25
 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
 30 35 40 45
 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
 50 55 60
 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
 65 70 75
 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
 80 85 90
 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu
 95 100 105
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Monkey

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: heavy variable domain of CE9.1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..387

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA 48
 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr
 -19 -15 -10 -5

GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG 96
 Asp Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val
 1 5 10

TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA 144
 Ser Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly
 15 20 25

AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG 192
 Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val
 30 35 40

CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA 240
 Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg
 45 50 55 60

TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG 288
 Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
 65 70 75

GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT 336
 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser
 80 85 90

ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA 384
 Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu
 95 100 105

GGT 387
 Gly

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
 -19 -15 -10 -5

Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
 1 5 10

Pro	Gly	Gln	Thr	Ala	Gly	Phe	Thr	Cys	Gly	Gly	Asp	Asn	Val	Gly	Arg	
		35					40					45				
AAA	AGT	GTA	CAG	TGG	TAC	CAG	CAG	AAG	CCA	CCG	CAG	GCC	CCT	GTG	CTG	192
Lys	Ser	Val	Gln	Trp	Tyr	Gln	Gln	Lys	Pro	Pro	Gln	Ala	Pro	Val	Leu	
	50					55					60					
GTC	ATC	TAT	GCT	GAC	AGC	GAA	CGG	CCC	TCA	GGG	ATC	CCT	GCG	CGA	TTC	240
Val	Ile	Tyr	Ala	Asp	Ser	Glu	Arg	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe	
	65				70					75					80	
TCT	GGC	TCC	AAC	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AGC	GGG	GTC	288
Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Val	
				85					90					95		
GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGT	ACT	336
Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Thr	
			100					105					110			
GCT	GAT	CAT	TGG	GTC	TTC	GGC	GGA	GGG	ACC	CGG	CTG	ACC	GTC	CTA	GGT	384
Ala	Asp	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly	
		115					120					125				
CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	GAG	432
Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	
	130					135					140					
GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	TTC	480
Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	
	145				150					155					160	
TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	GTC	528
Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	
				165				170						175		
AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	AAG	576
Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	
			180					185					190			
TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG	TCC	624
Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	
		195					200					205				
CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG	GAG	672
His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	
	210					215					220					
AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA							702
Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*							
	225				230											

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
 1 5 10 15
 Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
 20 25 30
 Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg
 35 40 45
 Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu
 50 55 60
 Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
 65 70 75 80
 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val
 85 90 95
 Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr
 100 105 110
 Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
 115 120 125
 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 130 135 140
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 145 150 155 160
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 165 170 175
 Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 180 185 190
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 195 200 205
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 210 215 220
 Lys Thr Val Ala Pro Thr Glu Cys Ser *
 225 230

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1404 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
 4

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1404

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCC	CCC	AGA	TGG	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		
GTC	TTG	TCC	CAG	GTG	CAG	CTG	CAG	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	
			20					25					30			
CCT	TCG	GAG	ACC	CTG	TCC	CTC	ACC	TGC	AGT	GTC	TCT	GGT	GGC	TCC	ATC	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	Ile	
		35					40					45				
AGC	GGT	GAC	TAT	TAT	TGG	TTC	TGG	ATC	CGC	CAG	TCC	CCA	GGG	AAG	GGA	192
Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	
	50					55					60					
CTG	GAG	TGG	ATC	GGC	TAC	ATC	TAT	GGC	AGT	GGT	GGG	GGC	ACC	AAT	TAC	240
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	
	65				70			75						80		
AAT	CCC	TCC	CTC	AAC	AAT	CGA	GTC	TCC	ATT	TCA	ATA	GAC	ACG	TCC	AAG	288
Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	
				85				90						95		
AAC	CTC	TTC	TCC	CTG	AAA	CTG	AGG	TCT	GTG	ACC	GCC	GCG	GAC	ACG	GCC	336
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	
			100					105					110			
GTC	TAT	TAC	TGT	GCG	AGT	AAT	ATA	TTG	AAA	TAT	CTT	CAC	TGG	TTA	TTA	384
Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	
		115					120					125				
TAC	TGG	GGC	CAG	GGA	GTC	CTG	GTC	ACC	GTC	TCC	TCA	GCT	AGC	ACC	AAG	432
Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	

355		360		365		
TAC ACC CTG CCC CCA TCC CAG GAG GAG ATG ACC AAG AAC CAG GTC AGC						1152
Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser						
370		375		380		
CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC GCC GTG GAG						1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu						
385		390		395		400
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC						1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro						
405				410		415
GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG						1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val						
420				425		430
GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC GTG ATG						1344
Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met						
435				440		445
CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT						1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser						
450				455		460
CTG GGT AAA TGA						1404
Leu Gly Lys *						
465						

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
 35 40 45
 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
 50 55 60
 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
 65 70 75 80

Asn	Pro	Ser	Leu	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	85	90	95	
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	100	105	110
Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	115	120	125
Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	130	135	140
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	145	150	155
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	165	170	175
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	180	185	190
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	195	200	205
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	210	215	220
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	225	230	235
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	245	250	255
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	260	265	270
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	275	280	285
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	290	295	300
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	305	310	315
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	325	330	335
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	340	345	350
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	355	360	365
Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	370	375	380

[illegible][illegible][illegible]

- [illegible]

[illegible][illegible]

- [illegible]

[illegible]

- [illegible]

[illegible]

- [illegible]

[illegible]

- [illegible]

[illegible]

ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCC	CCC	AGA	TGG	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		
GTC	TTG	TCC	CAG	GTG	CAG	CTG	CAG	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	
			20					25					30			
CCT	TCG	GAG	ACC	CTG	TCC	CTC	ACC	TGC	AGT	GTC	TCT	GGT	GGC	TCC	ATC	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	Ile	
		35					40					45				

AGC	GGT	GAC	TAT	TAT	TGG	TTC	TGG	ATC	CGC	CAG	TCC	CCA	GGG	AAG	GGA	192
Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	
	50					55					60					
CTG	GAG	TGG	ATC	GGC	TAC	ATC	TAT	GGC	AGT	GGT	GGG	GGC	ACC	AAT	TAC	240
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	
	65				70					75					80	
AAT	CCC	TCC	CTC	AAC	AAT	CGA	GTC	TCC	ATT	TCA	ATA	GAC	ACG	TCC	AAG	288
Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	
				85					90					95		
AAC	CTC	TTC	TCC	CTG	AAA	CTG	AGG	TCT	GTG	ACC	GCC	GCG	GAC	ACG	GCC	336
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	
			100					105					110			
GTC	TAT	TAC	TGT	GCG	AGT	AAT	ATA	TTG	AAA	TAT	CTT	CAC	TGG	TTA	TTA	384
Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	
		115					120					125				
TAC	TGG	GGC	CAG	GGA	GTC	CTG	GTC	ACC	GTC	TCC	TCA	GCT	AGC	ACC	AAG	432
Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	
	130					135					140					
GGG	CCA	TCC	GTC	TTC	CCC	CTG	GCG	CCC	TGC	TCC	AGG	AGC	ACC	TCC	GAG	480
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	
	145				150					155					160	
AGC	ACA	GCC	GCC	CTG	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	528
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
				165					170					175		
GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	576
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
			180				185						190			
TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	624
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	
		195					200					205				
GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACG	AAG	ACC	TAC	ACC	TGC	AAC	672
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	
	210					215					220					
GTA	GAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AGA	GTT	GAG	TCC	720
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	
	225					230				235					240	
AAA	TAT	GGT	CCC	CCA	TGC	CCA	TCA	TGC	CCA	GCA	CCT	GAG	TTC	GAG	GGG	768
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	
				245					250					255		
GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT	CTC	ATG	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260					265					270			

0007204T63T060

ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln 275 280 285	864
GAA GAC CCC GAG GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TTC AAC AGC ACG TAC His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 305 310 315 320	960
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAC GGC Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 340 345 350	1056
GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
TAC ACC CTG CCC CCA TCC CAG GAG GAG ATG ACC AAG AAC CAG GTC AGC Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 370 375 380	1152
CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC GCC GTG GAG Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 420 425 430	1296
GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC GTG ATG Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
CTG GGT AAA TGA Leu Gly Lys *	1404

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
 35 40 45
 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
 50 55 60
 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
 65 70 75 80
 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
 85 90 95
 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu
 115 120 125
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
 145 150 155 160
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
 210 215 220
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser
 225 230 235 240
 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Glu Gly
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
 275 280 285
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Leu Gly Lys *
 465

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E mutation

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1404

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
GTC TTG TCC CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile	
35 40 45	
AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG GGA	192
Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly	
50 55 60	
CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC	240
Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr	
65 70 75 80	
AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG	288
Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys	
85 90 95	
AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG GCC	336
Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala	
100 105 110	
GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA TTA	384
Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu	
115 120 125	
TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG	432
Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys	
130 135 140	
GGG CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG	480
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu	
145 150 155 160	
AGC ACA GCC GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG	528
Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro	

165										170					175					
GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC				576	
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr					
			180					185					190							
TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG				624	
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val					
		195					200					205								
GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACG	AAG	ACC	TAC	ACC	TGC	AAC				672	
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn					
		210				215					220									
GTA	GAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AGA	GTT	GAG	TCC				720	
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser					
		225				230				235					240					
AAA	TAT	GGT	CCC	CCA	TGC	CCA	CCA	TGC	CCA	GCA	CCT	GAG	TTC	GAG	GGG				768	
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly					
			245						250					255						
GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT	CTC	ATG				816	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met					
			260					265					270							
ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG				864	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln					
		275					280					285								
GAA	GAC	CCC	GAG	GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG				912	
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val					
		290				295					300									
CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TTC	AAC	AGC	ACG	TAC				960	
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr					
					310					315					320					
CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAC	GGC				1008	
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly					
				325					330					335						
AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC				1056	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile					
			340					345					350							
GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG				1104	
Glu	Lys	Thr																		

385	390	395	400	
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC				1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	405	410	415	
GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG				1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val	420	425	430	
GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC GTG ATG				1344
Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met	435	440	445	
CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT				1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	450	455	460	
CTG GGT AAA TGA				1404
Leu Gly Lys *				
465				

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	1	5	10	15
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	20	25	30	
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile	35	40	45	
Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly	50	55	60	
Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr	65	70	75	80
Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys	85	90	95	
Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala	100	105	110	
Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu				

000120-41627960

115 120 125
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
 145 150 155 160
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
 210 215 220
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser
 225 230 235 240
 Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
 245 250 255
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
 275 280 285
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415

(2) INFORMATION FOR SEQ ID NO:13:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

26

(i) SEQUENCE CHARACTERISTICS:

- (viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: VH2 leader sequence

ACTAAGTCGA CATGGACATA CTTTGTTCCA C

31

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH3 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTAAGTCGA CATGGAGTTT GGGCTGAGC

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH4 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTAAGTCGA CATGAAACAC CTGTGGTTCT T

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH5 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTAAGTCGA CATGGGGTCA ACCGCCATCC T

31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH6 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACTAAGTCGA CATGTCTGTC TCCTTCCTCA T

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

000123456789

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH1 leader sequence with MluI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCAGCAGCY ACGCGTGCCC ACTCCGAGGT

30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH2 leader sequence with MluI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GACCGTCCCG ACGCGTGTYT TGTCCCAGGT

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH3 leader sequence with MluI site

GCTATTTTCA CGCGTGTCCA GTGTGAG

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human or Monkey
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: VH4 leader sequence with MluI site

GCGGCTCCCA CGCGTGTCTT GTCCCAG

27

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human or Monkey
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: VH5 leader sequence with MluI site

GGCTGTTCTC ACGCGTGTCT GTGCCGAGGT

30

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs

(A) ORGANISM: Human or Monkey

(A) CHROMOSOME/SEGMENT: VH3b primer with XhoI site

GAGGTGCAGC TGCTCGAGTC TGG

23

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

(A) CHROMOSOME/SEGMENT: VH4 primer with XhoI site

CAGGTGCAGC TGCTCGAGTC GGG

23

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

(A) ORGANISM: Human or Monkey

(A) CHROMOSOME/SEGMENT: VH6 primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGTACAGC TGCTCGAGTC AGG

23

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: IgG1-4 primer with NheI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCGGATGCG CTAGCTGAGG AGACGG

26

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCACAGATC TCTACCATG GTGTTGCAGA CCCAGGTC

38

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(viii) POSITION IN GENOME:



ATCACAGATC TCTCACCATG GACACVAGGG CCCCCACTCA G

(2) INFORMATION FOR SEQ ID NO:34:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATCACAGATC TCTCACCATG GCCTGGGCTC TGCTGCTCC

39

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCACAGATC TCTCACCATG GCCTGGGCTC CACTACTTC

39

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATCACAGATC TCTCACCATG ACCTGCTCCC CTCTCCTCC

39

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCACAGATC TCTCACCATG GCCTGGACTC CTCTCTTTC

39

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (iv) ANTI-SENSE: YES

- (viii) POSITION IN GENOME:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: kappa light chain primer with Kpn1 and BsiW1 sites

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGCAGCATCC GTACGTTTGA TTTCCAGCTT

30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with HindIII and Kpn1 sites

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCTAGGACG GTAAGCTTGG TACCTCCGCC

30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Kpn 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCTAGGACG GTCASSTTGG TACCTCCGCC GAACAC

36

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with AvrII site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGGCTGA CCTAGGACGG TCAGCCG

27

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH1 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCATGGACTG GACCTGG

17

(2) INFORMATION FOR SEQ ID NO:45:

000720#4527960

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH2 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGGACATAC TTTGTTCCAC

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH3 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CCATGGAGTT TGGGCTGAGC

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH4 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATGAAACACC TGTGGTTCTT

20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH5 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATGGGGTCAA CCGCCATCCT

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH6 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATGTCTGTCT CCTTCCTCAT

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs

096344-4631960

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: IgM heavy chain constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTGGGGCGGA TGCACT

16

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: IgG1-4 heavy chain constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGGGCCCT TGGTGA

17

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: Kappa light chain variable region

00072044521950

21

21

19

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGAACAGAGT GACCGAGGGG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: PCR primer for human gamma 4 constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGGGATCC TCATTACCC AGAGACAGGG

30

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: PCR primer for Human gamma 4 constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGGGGCTAGC ACCAAGGGCC CATCCGTCTT C

31

(2) INFORMATION FOR SEQ ID NO:58:

0007204752960

- (A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: PCR mutagenesis of human gamma 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGGGAGATC ATGAGAGTGT CCTTGGGTTT TGGGGGGAAC AGGAAGACTG ATGGTCCCCC
CTCGAACTCA GGTGCTGGGC ATGGTGGGCA TGGGGG

60

96 .

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: PCR mutagenesis of human gamma 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TCCTCAGCTA GCACCAAGGG GCCATCC

27